pir|S11106|S11106), there were 18 substitution differences between residues 1 and 97, and 7 substitutions after residue 97.

- All other comparisons showed at least 14 substitution differences between residues 1 and 97.

- All other comparisons showed at least 3 substitution differences after residue 97.

- All other comparisons showed a total of at least 20 insertions, deletions and substitution differences.

- Differences appeared throughout the variable region.

Amino acid consensus sequences of the 15 most closely matched V_L and V_H regions were designed, and compared with the 1A7 sequences. This is shown in Figure 3(C). Other than splicing differences about the VDJ junction, there appear to be about 15 differences between 1A7 and the prototype sequences. Two of these differences are present in the light chain; 13 are present in the heavy chain. Seven occur in the CDRs, while nine occur in the variable region framework. The point differences likely have arisen from somatic mutation of germline variable region sequences.

In the claims

Please add new claims 90-99, as follows:

90. (New) A method of treating an individual with a GD2-associated tumor, comprising administering to the individual an effective amount of an antibody comprising the light and heavy chain variable region sequences contained in SEQ ID NO:2 and SEQ ID NO:4, respectively.

91. (New) The method of claim 90, wherein the GD2-associated tumor is melanoma.

92. (New) The method of claim 90, wherein said antibody is administered with an adjuvant.

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